MPsrch_pp protein - protein database search, using Smith-Waterman algorithm

Run: Wed Aug 16 09:45:05 2000; MasPar time 5.58 Seconds
560.903 Million cell updates/sec
Tabular output not generated.

Title: >US-09-427-873-2
Description: (1-101) from US09427873.pep
Perfect Score: 683
Sequence: 1 LGKFSQTCYNSAIQGSVLTS.....STKINLDDHIANIDGTLKYE 101

Scoring table: PAM 150
Gap 11

Searched: 85661 seqs, 30989116 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: swiss-prot38
1:swissprot

Statistics: Mean 39.367; Variance 62.654; scale 0.628

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description	Pred. No.
1	664	97.2	101	1	CVN_NOSEL	CYANOVIRIN-N (CV-N).	3.44e-138
2	103	15.1	327	1	ACCO_DORSP	1-AMINOCYCLOPROPANE-1-	3.79e-04
3	92	13.5	416	1	RHLA_PANTR	RH-LIKE PROTEIN IA (RH	2.79e-02
4	91	13.3	416	1	RHD_HUMAN	BLOOD GROUP RH(D) POLY	4.06e-02
5	91	13.3	505	1	ACHB_BOVIN	ACETYLCHOLINE RECEPTOR	4.06e-02
6	90	13.2	416	1	RHL_MACMU	RH-LIKE PROTEIN (RHESU	5.89e-02
7	89	13.0	416	1	RHLR_PANTR	RH-LIKE PROTEIN IIR (R	8.54e-02
8	86	12.6	353	1	RHL_HYLPI	RH-LIKE PROTEIN (RHESU	2.55e-01
9	86	12.6	392	1	VATC_YEAST	VACUOLAR ATP SYNTHASE	2.55e-01
10	86	12.6	1014	1	NANH_CLOSE	SIALIDASE PRECURSOR (E	2.55e-01
11	85	12.4	223	1	AOP2_MOUSE	ANTIOXIDANT PROTEIN 2	3.65e-01
12	85	12.4	223	1	AOP2_HUMAN	ANTIOXIDANT PROTEIN 2	3.65e-01
13	85	12.4	501	1	ACHB_RAT	ACETYLCHOLINE RECEPTOR	3.65e-01
14	85	12.4	501	1	ACHB_HUMAN	ACETYLCHOLINE RECEPTOR	3.65e-01
15	85	12.4	501	1	ACHB_MOUSE	ACETYLCHOLINE RECEPTOR	3.65e-01
16	84	12.3	223	1	AOX2_RAT	ANTIOXIDANT PROTEIN 2	5.21e-01
17	83	12.2	223	1	AOP2_BOVIN	ANTIOXIDANT PROTEIN 2	7.42e-01
18	83	12.2	416	1	RHLD_GORGO	RHESUS-LIKE PROTEIN.	7.42e-01
19	82	12.0	717	1	CLA1_ARATH	PROBABLE 1-DEOXYXYLULO	1.05e+00
20	81	11.9	320	1	ACC3_CUCME	1-AMINOCYCLOPROPANE-1-	1.49e+00
21	81	11.9	419	1	HFLK_ECOLI	HFLK PROTEIN.	1.49e+00
22	81	11.9	683	1	VTER_HSVSA	PROBABLE DNA PACKAGING	1.49e+00
23	80	11.7	450	1	ENVZ_ECOLI	OSMOLARITY SENSOR PROT	2.10e+00
24	80	11.7	470	1	ACHP_CHICK	NEURONAL ACETYLCHOLINE	2.10e+00
25	80	11.7	601	1	SG2_RANRI	SECRETOGRANIN II PRECU	2.10e+00
26	79	11.6	149	1	YGK6_YEAST	HYPOTHETICAL CALCIUM-B	2.95e+00
27	79	11.6	177	1	IDI_RHOSH	PROBABLE ISOPENTENYL-D	2.95e+00
28	79	11.6	318	1	ACC1_CUCME	1-AMINOCYCLOPROPANE-1-	2.95e+00
29	79	11.6	416	1	RHLF_PANTR	RH-LIKE PROTEIN IIF (R	2.95e+00
30	79	11.6	534	1	HTR2_NATPH	SENSORY RHODOPSIN II T	2.95e+00
31	79	11.6	706	1	BCL6_HUMAN	B-CELL LYMPHOMA 6 PROT	2.95e+00
32	79	11.6	845	1	SCP1_MESAU	SYNAPTONEMAL COMPLEX P	2.95e+00
33	79	11.6	845	1	CC47_YEAST	CELL DIVISION CONTROL	2.95e+00
34	79	11.6	3866	1	HRX_MOUSE	ZINC FINGER PROTEIN HR	2.95e+00
35	78	11.4	185	1	VP4_SBMV	P4 PROTEIN.	4.13e+00
36	78	11.4	307	1	CAH6_SHEEP	CARBONIC ANHYDRASE VI	4.13e+00
37	78	11.4	320	1	ACCO_PERAE	1-AMINOCYCLOPROPANE-1-	4.13e+00
38	78	11.4	416	1	RHLC_GORGO	RH-LIKE PROTEIN IC (RH	4.13e+00
39	78	11.4	442	1	FLGE_BORBU	FLAGELLAR HOOK PROTEIN	4.13e+00
40	78	11.4	450	1	ENVZ_SALTY	OSMOLARITY SENSOR PROT	4.13e+00
41	78	11.4	450	1	ENVZ_SALTI	OSMOLARITY SENSOR PROT	4.13e+00
42	78	11.4	960	1	DLG1_DROME	LETHAL(1)DISCS LARGE-1	4.13e+00
43	78	11.4	1238	1	BVGS_BORBR	VIRULENCE SENSOR PROTE	4.13e+00
44	78	11.4	1238	1	BVGS_BORPA	VIRULENCE SENSOR PROTE	4.13e+00
45	78	11.4	2249	1	190K_RICRI	190 KDA ANTIGEN PRECUR	4.13e+00

ALIGNMENTS

```
RESULT    1
ID   CVN_NOSEL      STANDARD;      PRT;   101 AA.
AC   P81180;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   CYANOVIRIN-N (CV-N).
OS   Nostoc ellipsosporum.
OC   Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
RN   [1]
RP   SEQUENCE.
RX   MEDLINE; 97445156.
RA   Gustafson K.R., Sowder R.C. II, Henderson L.E., Cardellina J.H. II,
RA   McMahon J.B., Rajamani U., Pannell L.K., Boyd M.R.;
RT   "Isolation, primary sequence determination, and disulfide bond
RT   structure of cyanovirin-N, an anti-HIV (human immunodeficiency virus)
RT   protein from the cyanobacterium Nostoc ellipsosporum.";
RL   Biochem. Biophys. Res. Commun. 238:223-228(1997).
RN   [2]
RP   X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX   MEDLINE; 99262850.
RA   Yang F., Bewley C.A., Louis J.M., Gustafson K.R., Boyd M.R.,
RA   Gronenborn A.M., Clore G.M., Wlodawer A.;
RT   "Crystal structure of cyanovirin-N, a potent HIV-inactivating protein,
RT   shows unexpected domain swapping.";
RL   J. Mol. Biol. 288:403-412(1999).
CC   -!- FUNCTION: CAPABLE OF INHIBITING HIV-1 AND HIV-2 INFECTION AND
CC       REPLICATION.
CC   -!- MISCELLANEOUS: CLEAVAGE OF THE DISULFIDE BONDS RESULTS IN THE LOSS
CC       OF ANTI-HIV ACTIVITY.
DR   PDB; 3EZM; 23-DEC-98.
KW   Antiviral; Protein synthesis inhibitor; 3D-structure.
FT   DISULFID      8     22
FT   DISULFID     58     73
SQ   SEQUENCE   101 AA;  11013 MW;  1F84E5B886CCE973 CRC64;

  Query Match           97.2%;  Score 664;  DB 1;  Length 101;
  Best Local Similarity 98.0%;  Pred. No. 3.44e-138;
  Matches   99;  Conservative    0;  Mismatches   2;  Indels   0;  Gaps   0;

Db      1 LGKFSQTCYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVEINVDGSLKWQPSNFIETCRN 60
          ||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||
Qy      1 LGKFSQTCYNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIENVDGSLKWQPSNFIETCRN 60

Db     61 TQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE 101
          |||||||||||||||||||||||||||||||||||||||||
Qy     61 TQLAGSSELAAECKTRAQQFVSTKINLDDHIANIDGTLKYE 101
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RESULT    2
ID   ACCO_DORSP     STANDARD;      PRT;   327 AA.
AC   P31238;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUL-1993 (Rel. 26, Last sequence update)
DT   15-FEB-2000 (Rel. 39, Last annotation update)
DE   1-AMINOCYCLOPROPANE-1-CARBOXYLATE OXIDASE (EC 1.-.-.-) (ACC OXIDASE)
DE   (ETHYLENE-FORMING ENZYME) (EFE).
GN   ACO.
OS   Doritaenopsis sp. (Moth orchid).
OC   Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC   Magnoliophyta; Liliopsida; Asparagales; Orchidaceae; Doritaenopsis.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94269201.
RA   Nadeau J.A., Zhang X., Nair H., O'Neill S.D.;
RT   "Temporal and spatial regulation of 1-aminocyclopropane-1-carboxylate
RT   oxidase in the pollination-induced senescence of orchid flowers.";
RL   Plant Physiol. 103:31-39(1993).
CC   -!- CATALYTIC ACTIVITY: 1-AMINOCYCLOPROPANE-1-CARBOXYLATE + O2 =
CC       ETHYLENE + HCN + CO(2) + 2 H(2)O.
CC   -!- COFACTOR: IRON AND ASCORBATE.
CC   -!- PATHWAY: LAST STEP IN THE BIOSYNTHESIS OF ETHYLENE.
CC   -!- SIMILARITY: BELONGS TO THE IRON/ASCORBATE-DEPENDENT FAMILY OF
CC       OXIDOREDUCTASES.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L07912; -; NOT_ANNOTATED_CDS.
DR   MENDEL; 8019; DORsp;Aco;1.
DR   PFAM; PF00671; Fe_Asc_oxidored; 1.
KW   Fruit ripening; Ethylene biosynthesis; Oxidoreductase; Iron;
KW   Vitamin C; Multigene family.
SQ   SEQUENCE   327 AA;  37233 MW;  D4EC83D9971059EE CRC64;

  Query Match           15.1%;  Score 103;  DB 1;  Length 327;
  Best Local Similarity  21.9%;  Pred. No. 3.79e-04;
  Matches   14;  Conservative   23;  Mismatches  25;  Indels   2;  Gaps   2;

Db     71 ASKTLDTV-ENVEPENLDWESTFFLRHLPTSNISQIPDLDDDCRSTMKEFALELENLAER 129
           :|  |::| |||:  :| |::: |:     : ::  ::|  :|::   :|     || ::
Qy     32 SSIDLNSVIENVD-GSLKWQPSNFIETCRNTQLAGSSELAAECKTRAQQFVSTKINLDDH 90

Db    130 LLDL 133
          : ::
Qy     91 IANI 94


RESULT    3
ID   RHLA_PANTR     STANDARD;      PRT;   416 AA.
AC   Q28813;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RH-LIKE PROTEIN IA (RHESUS-LIKE PROTEIN IA).
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE; 95085595.
RA   Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
RA   Colin Y., Ruffie J.;
RT   "Molecular genetics of chimpanzee Rh-related genes: their
RT   relationship with the R-C-E-F blood group system, the chimpanzee
RT   counterpart of the human rhesus system.";
RL   Biochem. Genet. 32:201-221(1994).
CC   -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
CC       HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE RH FAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L37049; AAA65623.1; -.
DR   PFAM; PF00909; Ammonium_transp; 1.
DR   PRINTS; PR00342; RHESUSRHD.
KW   Erythrocyte; Transmembrane.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     43     63       POTENTIAL.
FT   TRANSMEM     76     96       POTENTIAL.
FT   TRANSMEM    124    144       POTENTIAL.
FT   TRANSMEM    171    191       POTENTIAL.
FT   TRANSMEM    202    222       POTENTIAL.
FT   TRANSMEM    237    257       POTENTIAL.
FT   TRANSMEM    264    284       POTENTIAL.
FT   TRANSMEM    286    306       POTENTIAL.
FT   TRANSMEM    330    350       POTENTIAL.
FT   TRANSMEM    357    377       POTENTIAL.
SQ   SEQUENCE   416 AA;  45461 MW;  B0B566734DB5E14D CRC64;

  Query Match           13.5%;  Score 92;  DB 1;  Length 416;
  Best Local Similarity  23.7%;  Pred. No. 2.79e-02;
  Matches   22;  Conservative   30;  Mismatches  36;  Indels   5;  Gaps   5;

Db    220 PSFNSALLRSPIERKNAVFNTYYAVAV-SVVTAISGSSLAHPQGKISMSYMHNAVLAGGV 278
          ::: :::| |  || |: :||  :: : ||:  : || |    :::  :  :|: |||:
Qy     11 SAIQGSVLTSTCERTNGGYNTS-SIDLNSVIENVDGS-LKWQPSNFIETC-RNTQLAGSS 67

Db    279 AVGTSCHLITSPWLAMVLGLVAGLISIGGA-KY 310
          ::: |   :   ::  : |   : :| |: ||
Qy     68 ELAAECKTRAQQFVSTKINLDDHIANIDGTLKY 100


RESULT    4
ID   RHD_HUMAN      STANDARD;      PRT;   416 AA.
AC   Q02161; Q02162; Q07618; Q16355; Q16147; Q16235;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   15-FEB-2000 (Rel. 39, Last annotation update)
DE   BLOOD GROUP RH(D) POLYPEPTIDE (RHESUS D ANTIGEN) (RHXIII) (RH
DE   POLYPEPTIDE 2) (RHPII).
GN   RHD.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE; 93066356.
RA   le van Kim C., Mouro I., Cherif-Zahar B., Raynal V., Cherrier C.,
RA   Cartron J.-P., Colin Y.;
RT   "Molecular cloning and primary structure of the human blood group RhD
RT   polypeptide.";
RL   Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE; 92360855.
RA   le van Kim C., Cherif-Zahar B., Raynal V., Mouro I., Lopez M.,
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RA   Cartron J.-P., Colin Y.;
RT   "Multiple Rh messenger RNA isoforms are produced by alternative
RT   splicing.";
RL   Blood 80:1074-1078(1992).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93320449.
RA   Arce M.A., Thompson E.S., Wagner S., Coyne K.E., Ferdman B.A.,
RA   Lublin D.M.;
RT   "Molecular cloning of RhD cDNA derived from a gene present in RhD-
RT   positive, but not RhD-negative individuals.";
RL   Blood 82:651-655(1993).
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 93216282.
RA   Kajii E., Umenishi F., Iwamoto S., Ikemoto S.;
RT   "Isolation of a new cDNA clone encoding an Rh polypeptide associated
RT   with the Rh blood group system.";
RL   Hum. Genet. 91:157-162(1993).
RN   [5]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 95329738.
RA   Huang C.H., Reid M.E., Chen Y.;
RT   "Identification of a partial internal deletion in the RH locus
RT   causing the human erythrocyte D-phenotype.";
RL   Blood 86:784-790(1995).
RN   [6]
RP   SEQUENCE FROM N.A. (SHORT FORM 1).
RX   MEDLINE; 94235883.
RA   Westhoff C.M., Wylie D.E.;
RT   "Identification of a new RhD-specific mRNA from K562 cells.";
RL   Blood 83:3098-3100(1994).
RN   [7]
RP   SEQUENCE FROM N.A. (SHORT FORM 2).
RX   MEDLINE; 94362249.
RA   Suyama K., Lunn R., Haller S., Goldstein J.;
RT   "Rh(D) antigen expression and isolation of a new Rh(D) cDNA isoform
RT   in human erythroleukemic K562 cells.";
RL   Blood 84:1975-1981(1994).
RN   [8]
RP   VARIANT BLOOD GROUP TAR.
RX   MEDLINE; 95259709.
RA   Rouillac C., le van Kim C., Beolet M., Cartron J.-P., Colin Y.;
RT   "Leu110Pro substitution in the RhD polypeptide is responsible for the
RT   DVII category blood group phenotype.";
RL   Am. J. Hematol. 49:87-88(1995).
CC   -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
CC       HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- ALTERNATIVE PRODUCTS: VARIOUS FORMS ARE PRODUCED BY ALTERNATIVE
CC       SPLICING.
CC   -!- TISSUE SPECIFICITY: RESTRICTED TO TISSUES OR CELL LINES EXPRESSING
CC       ERYTHROID CHARACTERS.
CC   -!- POLYMORPHISM: RHD AND RHCE ARE RESPONSIBLE FOR THE RH BLOOD GROUP
CC       SYSTEM. THE MOLECULAR BASIS OF THE TAR=RH40 BLOOD GROUP ANTIGEN
CC       IS A POLYMORPHISM IN POSITION 109.
CC   -!- SIMILARITY: BELONGS TO THE RH FAMILY. STRONG, TO RHCE.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X63097; CAA44811.1; -.
DR   EMBL; X63094; CAA44808.1; -.
DR   EMBL; L08429; AAA02679.1; -.
DR   EMBL; S57971; AAB26081.1; -.
DR   EMBL; S78509; AAB34852.1; -.
DR   EMBL; S70174; AAB30756.1; -.
DR   EMBL; S73913; AAB31911.1; -.
DR   PIR; S26564; S26564.
DR   MIM; 111680; -.
DR   PFAM; PF00909; Ammonium_transp; 1.
DR   PRINTS; PR00342; RHESUSRHD.
KW   Erythrocyte; Transmembrane; Blood group antigen; Alternative splicing;
KW   Polymorphism.
FT   INIT_MET      0      0
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     43     63       POTENTIAL.
FT   TRANSMEM     76     96       POTENTIAL.
FT   TRANSMEM    106    126       POTENTIAL.
FT   TRANSMEM    129    149       POTENTIAL.
FT   TRANSMEM    166    186       POTENTIAL.
FT   TRANSMEM    202    222       POTENTIAL.
FT   TRANSMEM    237    257       POTENTIAL.
FT   TRANSMEM    286    306       POTENTIAL.
FT   TRANSMEM    333    353       POTENTIAL.
FT   TRANSMEM    357    377       POTENTIAL.
FT   VARSPLIC    313    408       MISSING (IN SHORT ISOFORM 1).
FT   VARSPLIC    315    315       C -> S (IN SHORT ISOFORM 2).
FT   VARSPLIC    316    416       MISSING (IN SHORT ISOFORM 2).
FT   VARIANT     109    109       L -> P (IN TAR ANTIGEN).
FT                                /FTId=VAR_006919.
FT   VARIANT     217    217       M -> I.
FT                                /FTId=VAR_006920.
FT   CONFLICT     15     15       W -> C (IN REF. 5).
FT   CONFLICT     38     38       E -> G (IN REF. 4).
FT   CONFLICT    102    102       S -> P (IN REF. 4).
FT   CONFLICT    126    126       V -> A (IN REF. 4).
FT   CONFLICT    173    173       V -> M (IN REF. 5).
FT   CONFLICT    181    181       S -> T (IN REF. 4).
FT   CONFLICT    313    313       G -> V (IN REF. 4 AND 7).
FT   CONFLICT    322    322       P -> H (IN REF. 4).
FT   CONFLICT    397    397       E -> V (IN REF. 5).
SQ   SEQUENCE   416 AA;  45049 MW;  9136DF1A37D76B1B CRC64;

  Query Match           13.3%;  Score 91;  DB 1;  Length 416;
  Best Local Similarity  22.6%;  Pred. No. 4.06e-02;
  Matches   21;  Conservative   31;  Mismatches  36;  Indels   5;  Gaps   5;

Db    220 PSFNSALLRSPIERKNAVFNTYYAVAV-SVVTAISGSSLAHPQGKISKTYVHSAVLAGGV 278
          ::: :::| |  || |: :||  :: : ||:  : || |    :::  |  ::: |||:
Qy     11 SAIQGSVLTSTCERTNGGYNTS-SIDLNSVIENVDGS-LKWQPSNFIETC-RNTQLAGSS 67

Db    279 AVGTSCHLIPSPWLAMVLGLVAGLISVGGA-KY 310
           ::: |   :   ::  : |   : :: |: ||
Qy     68 ELAAECKTRAQQFVSTKINLDDHIANIDGTLKY 100


RESULT    5
ID   ACHB_BOVIN     STANDARD;      PRT;   505 AA.
AC   P04758;
DT   13-AUG-1987 (Rel. 05, Created)
DT   13-AUG-1987 (Rel. 05, Last sequence update)
DT   01-OCT-1996 (Rel. 34, Last annotation update)
DE   ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
GN   CHRNB1.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 85003649.
RA   Tanabe T., Noda M., Furutani Y., Takai T., Takahashi H., Tanaka K.,
RA   Hirose T., Inayama S., Numa S.;
RT   "Primary structure of beta subunit precursor of calf muscle
RT   acetylcholine receptor deduced from cDNA sequence.";
RL   Eur. J. Biochem. 144:11-17(1984).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
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CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X00962; CAA25475.1; -.
DR   PIR; S07227; S07227.
DR   PFAM; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00254; NICOTINICR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Phosphorylation.
FT   SIGNAL        1     24
FT   CHAIN        25    505       ACETYLCHOLINE RECEPTOR PROTEIN, BETA
FT                                 CHAIN.
FT   DOMAIN        25    245       EXTRACELLULAR.
FT   TRANSMEM     246    270
FT   TRANSMEM     278    295
FT   TRANSMEM     312    333
FT   DOMAIN       334    473       CYTOPLASMIC.
FT   TRANSMEM     474    492
FT   DISULFID     152    166       BY SIMILARITY.
FT   CARBOHYD     165    165       PROBABLE.
FT   MOD_RES      394    394       PHOSPHORYLATION (BY TYR-KINASES)
FT                                 (BY SIMILARITY).
SQ   SEQUENCE   505 AA;  57352 MW;  B003D552A6701ECC CRC64;

  Query Match           13.3%;  Score 91;  DB 1;  Length 505;
  Best Local Similarity  32.4%;  Pred. No. 4.06e-02;
  Matches    11;  Conservative   13;  Mismatches   7;  Indels   3;  Gaps   3;

Db    121 DGNFDVA-LDINVVVSS-DGSMRWQPPGIYRSSC 152
          :| :: : :|:| |: : |||::|||:  :  :|
Qy     26 NGGYNTSSIDLNSVIENVDGSLKWQPSN-FIETC 58


RESULT    6
ID   RHL_MACMU      STANDARD;      PRT;   416 AA.
AC   Q28849;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RH-LIKE PROTEIN (RHESUS-LIKE PROTEIN).
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE; 94223693.
RA   Mouro I., le van Kim C., Cherif-Zahar B., Salvignol I., Blancher A.,
RA   Cartron J.-P., Colin Y.;
RT   "Molecular characterization of the Rh-like locus and gene transcripts
RT   from the rhesus monkey (Macaca mulatta).";
RL   J. Mol. Evol. 38:169-176(1994).
CC   -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
CC       HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE RH FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; S70343; AAB30637.1; -.
DR   PFAM; PF00909; Ammonium_transp; 1.
DR   PRINTS; PR00342; RHESUSRHD.
KW   Erythrocyte; Transmembrane; Polymorphism.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     43     63       POTENTIAL.
FT   TRANSMEM     76     96       POTENTIAL.
FT   TRANSMEM    124    144       POTENTIAL.
FT   TRANSMEM    171    191       POTENTIAL.
FT   TRANSMEM    202    222       POTENTIAL.
FT   TRANSMEM    237    257       POTENTIAL.
FT   TRANSMEM    264    284       POTENTIAL.
FT   TRANSMEM    286    306       POTENTIAL.
FT   TRANSMEM    330    350       POTENTIAL.
FT   TRANSMEM    357    377       POTENTIAL.
FT   VARIANT       1     55       MISSING (IN MAC-B).
FT   VARIANT      70     70       R -> K (IN MAC-B).
FT   VARIANT     106    106       A -> V (IN MAC-B).
FT   VARIANT     191    191       P -> L (IN MAC-B).
FT   VARIANT     261    261       G -> R (IN MAC-B).
FT   VARIANT     342    342       Y -> C (IN MAC-B).
SQ   SEQUENCE   416 AA;  45672 MW;  3BFD939BEA79AF6F CRC64;

  Query Match           13.2%;  Score 90;  DB 1;  Length 416;
  Best Local Similarity  23.3%;  Pred. No. 5.89e-02;
  Matches    21;  Conservative   29;  Mismatches  36;  Indels   4;  Gaps   4;

Db    220 PTFNSALLLNPIERKNAVFSTYYALAVSAVTAISVSSLA-HPGGKINMTYMHNAALAGGV 278
          ::: :::| :  || |: ::|  :: :::|     :||  :|:  |: |  :|: |||:
Qy     11 SAIQGSVLTSTCERTNGGYNTS-SIDLNSVIENVDGSLKWQPSNFIE-TC-RNTQLAGSS 67

Db    279 ALSASCHVIHSPWIAMVLGLVAGLISIGGA 308
           |:| |       ::  : |   : :| |:
Qy     68 ELAAECKTRAQQFVSTKINLDDHIANIDGT 97


RESULT    7
ID   RHLR_PANTR     STANDARD;      PRT;   416 AA.
AC   Q28814;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RH-LIKE PROTEIN IIR (RHESUS-LIKE PROTEIN IIR).
OS   Pan troglodytes (Chimpanzee).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE; 95085595.
RA   Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
RA   Colin Y., Ruffie J.;
RT   "Molecular genetics of chimpanzee Rh-related genes: their
RT   relationship with the R-C-E-F blood group system, the chimpanzee
RT   counterpart of the human rhesus system.";
RL   Biochem. Genet. 32:201-221(1994).
CC   -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
CC       HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE RH FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; L37050; AAA65624.1; -.
DR   PFAM; PF00909; Ammonium_transp; 1.
DR   PRINTS; PR00342; RHESUSRHD.
KW   Erythrocyte; Transmembrane.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   TRANSMEM     11     31       POTENTIAL.
FT   TRANSMEM     43     63       POTENTIAL.
FT   TRANSMEM     76     96       POTENTIAL.
FT   TRANSMEM    124    144       POTENTIAL.
FT   TRANSMEM    171    191       POTENTIAL.
FT   TRANSMEM    202    222       POTENTIAL.
FT   TRANSMEM    237    257       POTENTIAL.
FT   TRANSMEM    264    284       POTENTIAL.
FT   TRANSMEM    286    306       POTENTIAL.
FT   TRANSMEM    330    350       POTENTIAL.
FT   TRANSMEM    357    377       POTENTIAL.
SQ   SEQUENCE   416 AA;  45299 MW;  C055D7CC8B4A0420 CRC64;

  Query Match           13.0%;  Score 89;  DB 1;  Length 416;
  Best Local Similarity  22.6%;  Pred. No. 8.54e-02;
  Matches    21;  Conservative   31;  Mismatches  36;  Indels   5;  Gaps   5;

Db    220 PSFNSALLRSPIERKNAVFNTYYAVAV-SVVTAISGSSLAHPQGKISMSYMHNAVLAGGV 278
          ::: :::| |  || |: :||  :: : ||:  : || |    :::  :  :|: |||:
Qy     11 SAIQGSVLTSTCERTNGGYNTS-SIDLNSVIENVDGS-LKWQPSNFIETC-RNTQLAGSS 67

Db    279 AVGTSCHLIPSPWLAMVLGLVAGLISVGGA-KY 310
            ::: |   :   ::  : |   : :: |: ||
Qy     68 ELAAECKTRAQQFVSTKINLDDHIANIDGTLKY 100


RESULT    8
ID   RHL_HYLPI      STANDARD;      PRT;   353 AA.
AC   Q28446;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   RH-LIKE PROTEIN (RHESUS-LIKE PROTEIN).
OS   Hylobates pileatus (Pileated gibbon).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=BONE MARROW;
RX   MEDLINE; 95085595.
RA   Salvignol I., Blancher A., Calvas P., Clayton J., Socha W.W.,
RA   Colin Y., Ruffie J.;
RT   "Molecular genetics of chimpanzee Rh-related genes: their
RT   relationship with the R-C-E-F blood group system, the chimpanzee
RT   counterpart of the human rhesus system.";
RL   Biochem. Genet. 32:201-221(1994).
CC   -!- FUNCTION: MAY BE PART OF AN OLIGOMERIC COMPLEX WHICH IS LIKELY TO
CC       HAVE A TRANSPORT OR CHANNEL FUNCTION IN THE ERYTHROCYTE MEMBRANE.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE RH FAMILY.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; L37051; AAA65625.1; -.
DR   PFAM; PF00909; Ammonium_transp; 1.
KW   Erythrocyte; Transmembrane.
FT   INIT_MET      0      0       BY SIMILARITY.
FT   TRANSMEM     10     30       POTENTIAL.
FT   TRANSMEM     44     64       POTENTIAL.
FT   TRANSMEM     76     96       POTENTIAL.
FT   TRANSMEM    124    144       POTENTIAL.
FT   TRANSMEM    166    186       POTENTIAL.
FT   TRANSMEM    208    228       POTENTIAL.
FT   TRANSMEM    237    257       POTENTIAL.
FT   TRANSMEM    286    306       POTENTIAL.
SQ   SEQUENCE   353 AA;  38417 MW;  3CFD25B38033AB6A CRC64;

  Query Match           12.6%;  Score 86;  DB 1;  Length 353;
  Best Local Similarity  21.3%;  Pred. No. 2.55e-01;
  Matches    19;  Conservative   31;  Mismatches  37;  Indels   2;  Gaps   2;

Db    220 PSFNSALLTNPIERKNAVFNTYYALAVSTVTAISVSSLAHPQGKINMTYMHNAVLAGGVA 279
          ::: :::||:  || |: :||  :: :::|     :||    :::  |  :|: |||:
Qy     11 SAIQGSVLTSTCERTNGGYNTS-SIDLNSVIENVDGSLKWQPSNFIETC-RNTQLAGSSE 68

Db    280 VGTSCHLISSPWLAMVLGLVAGLISIGGA 308
          ::: |   :   ::  : |   : :| |:
Qy     69 LAAECKTRAQQFVSTKINLDDHIANIDGT 97


RESULT    9
ID   VATC_YEAST     STANDARD;      PRT;   392 AA.
AC   P31412;
DT   01-JUL-1993 (Rel. 26, Created)
DT   01-JUN-1994 (Rel. 29, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   VACUOLAR ATP SYNTHASE SUBUNIT C (EC 3.6.1.34) (V-ATPASE C SUBUNIT)
DE   (V-ATPASE 42 KDA SUBUNIT).
GN   VMA5 OR VAT3 OR VATC OR YKL080W OR YKL410.
OS   Saccharomyces cerevisiae (Baker's yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;
OC   Saccharomycetaceae; Saccharomyces.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 99-117.
RX   MEDLINE; 92112808.
RA   Beltran C., Kopecky J., Pan Y.-C.E., Nelson H., Nelson N.;
RT   "Cloning and mutational analysis of the gene encoding subunit C of
RT   yeast vacuolar H(+)-ATPase.";
RL   J. Biol. Chem. 267:774-779(1992).
RN   [2]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE; 93107006.
RA   Ho M.N., Hill K.J., Lindorfer M.A., Stevens T.H.;
RT   "Isolation of vacuolar membrane H(+)-ATPase-deficient yeast mutants;
RT   the VMA5 and VMA4 genes are essential for assembly and activity of
RT   the vacuolar H(+)-ATPase.";
RL   J. Biol. Chem. 268:221-227(1993).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Pohl T.M., Pohl F.M.;
RL   Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 94262328.
RA   James C.M., Gent M.E., Indge K.J., Oliver S.G.;
RT   "Sequence analysis of a 10 kb fragment of yeast chromosome XI
RT   identifies the SMY1 locus and reveals sequences related to a pre-mRNA
RT   splicing factor and vacuolar ATPase subunit C plus a number of
RT   unidentified open reading frames.";
RL   Yeast 10:247-255(1994).
CC   -!- FUNCTION: SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF VACUOLAR ATPASE.
CC       SUBUNIT C IS NECESSARY FOR THE ASSEMBLY OF THE CATALYTIC SECTOR OF
CC       THE ENZYME AND IS LIKELY TO HAVE A SPECIFIC FUNCTION IN ITS
CC       CATALYTIC ACTIVITY. V-ATPASE IS RESPONSIBLE FOR ACIDIFYING A
CC       VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC CELLS.
CC   -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
CC       PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
CC       C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
CC       COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).
CC   -!- SIMILARITY: TO V-ATPASE SUBUNIT C FROM OTHER SPECIES.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; M77143; AAA34440.1; -.
DR   EMBL; X75560; CAA53237.1; -.
DR   EMBL; Z28080; CAA81917.1; -.
DR   PIR; S37905; S37905.
DR   PIR; S39118; S39118.
DR   SGD; L0002460; VMA5.
KW   Hydrolase; Hydrogen ion transport.
FT   CONFLICT       1      25       MATALYTANDFILISLPQNAQPVTA -> MLNLLR (IN
FT                                  REF. 1 AND 2).
SQ   SEQUENCE   392 AA;  44188 MW;  0CD1B814046C377E CRC64;

  Query Match           12.6%;  Score 86;  DB 1;  Length 392;
  Best Local Similarity  24.1%;  Pred. No. 2.55e-01;
  Matches    21;  Conservative   24;  Mismatches  36;  Indels   6;  Gaps   6;

Db      85 ILQGLNETSTNAYRTLPINNMPVPEYLE-NFQWQTRKFKLDKSIKDLITLISNESSQLDA 143
           :| :  | :  :| | :|:  :| | :: :: ||  :| ::   ::   | :  ||:| |
Qy      17 VLTSTCERTNGGYNTSSIDLNSVIENVDGSLKWQPSNF-IETC-RN-TQL-AG-SSELAA 71

Db     144 DVRATYANYNSAKTNLAAAERKKTGDL 170
           : ::    : |:| ||     :  | |
Qy      72 ECKTRAQQFVSTKINLDDHIANIDGTL 98


RESULT   10
ID   NANH_CLOSE     STANDARD;      PRT;  1014 AA.
AC   P29767;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-APR-1993 (Rel. 25, Last sequence update)
DT   01-OCT-1994 (Rel. 30, Last annotation update)
DE   SIALIDASE PRECURSOR (EC 3.2.1.18) (NEURAMINIDASE).
OS   Clostridium septicum.
OC   Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;
OC   Clostridium.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=NC 0054714;
RX   MEDLINE; 91238693.
RA   Rothe B., Rothe B., Roggentin P., Schauer R.;
RT   "The sialidase gene from Clostridium septicum: cloning, sequencing,
RT   expression in Escherichia coli and identification of conserved
RT   sequences in sialidases and other proteins.";
RL   Mol. Gen. Genet. 226:190-197(1991).
CC   -!- FUNCTION: SIALIDASES HAVE BEEN SUGGESTED TO BE PATHOGENIC FACTORS
CC       IN MICROBIAL INFECTIONS.
CC   -!- CATALYTIC ACTIVITY: HYDROLYSIS OF 2,3-, 2,6- AND 2,8-GLYCOSIDIC
CC       LINKAGES JOINING TERMINAL NON-REDUCING N- OR O-ACYLNEURAMINYL
CC       RESIDUES TO GALACTOSE, N-ACETYLHEXOSAMINE, OR N- OR O-ACYLATED
CC       NEURAMINYL RESIDUES IN OLIGOSACCHARIDES, GLYCOPROTEINS,
CC       GLYCOLIPIDS OR COLOMINIC ACID.
CC   -!- SUBCELLULAR LOCATION: PERIPLASMIC.
CC   -!- SIMILARITY: BELONGS TO FAMILY 33 OF GLYCOSYL HYDROLASES.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; X63266; CAA44916.1; -.
DR   PIR; S15994; NMCLSS.
DR   HSSP; Q02834; 1EUS.
DR   PFAM; PF02012; BNR; 4.
KW   Hydrolase; Glycosidase; Periplasmic; Signal; Repeat.
FT   SIGNAL         1     26       POTENTIAL.
FT   CHAIN         27   1014       SIALIDASE.
FT   REPEAT       431    442       BNR MOTIF.
FT   REPEAT       563    574       BNR MOTIF.
FT   REPEAT       627    638       BNR MOTIF.
FT   REPEAT       700    711       BNR MOTIF.
SQ   SEQUENCE   1014 AA;  110652 MW;  C4F49233473A2FAD CRC64;

  Query Match           12.6%;  Score 86;  DB 1;  Length 1014;
  Best Local Similarity  27.1%;  Pred. No. 2.55e-01;
  Matches    13;  Conservative   20;  Mismatches  12;  Indels   3;  Gaps   3;

Db     401 Y-TTKDGTVLASIDVRKGGGHDAPN-NIDTGIKRSTDGGVTWDEGKII 446
           | :: :|:||:|   |  || :::: :::: |  : ||:: |: :::|
Qy       9 YNSAIQGSVLTSTCERTNGGYNTSSIDLNSVIE-NVDGSLKWQPSNFI 55


RESULT   11
ID   AOP2_MOUSE     STANDARD;      PRT;   223 AA.
AC   O08709;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-JUL-1999 (Rel. 38, Last annotation update)
DE   ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (NONSELENIUM GLUTATHIONE
DE   PEROXIDASE) (1-CYS PEROXIREDOXIN) (1-CYS PRX).
GN   AOP2 OR LTW4.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-25.
RC   STRAIN=DBA/2J, C57BL/6J, AND C3H/FEJ; TISSUE=LIVER, AND KIDNEY;
RX   MEDLINE; 97349116.
RA   Iakoubova O.A., Pacella L.A., Her H., Beier D.R.;
RT   "LTW4 protein on mouse chromosome 1 is a member of a family of
RT   antioxidant proteins.";
RL   Genomics 42:474-478(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/C; TISSUE=SKIN;
RX   MEDLINE; 97419117.
RA   Munz B., Frank S., Huebner G., Olsen E., Werner S.;
RT   "A novel type of glutathione peroxidase: expression and regulation
RT   during wound repair.";
RL   Biochem. J. 326:579-585(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6;
RA   Lee T.H., Yu S.L., Kim S.Y., Kang S.W., Rhee S.G., Seong J.K.,
RA   Yu D.Y.;
RT   "Characterization of the murine gene encoding 1-Cys peroxiredoxin and
RT   identification of highly homologous genes.";
RL   Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC   -!- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN HEART, KIDNEY AND LIVER.
CC       MODERATE EXPRESSION IN BRAIN AND STOMACH. VERY LOW LEVELS IN
CC       INTESTINE.
CC   -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. REHYDRIN SUBFAMILY.
CC   ---------------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; AF004670; AAC53277.1; -.
DR   EMBL; Y12883; CAA73383.1; -.
DR   EMBL; AF093852; AAC63376.1; -.
DR   HSSP; P30041; 1PRX.
DR   SWISS-2DPAGE; O08709; MOUSE.
DR   MGD; MGI:894320; AOP2.
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DR   PFAM; PF00578; AhpC-TSA; 1.
KW   Oxidoreductase; Peroxidase; Antioxidant.
FT   INIT_MET      0      0
FT   ACT_SITE     46     46       BY SIMILARITY.
FT   VARIANT     123    123       D -> A (IN C57BL/6J).
SQ   SEQUENCE   223 AA;  24739 MW;  A4F2B1E36180BBCF CRC64;

  Query Match           12.4%;  Score 85;  DB 1;  Length 223;
  Best Local Similarity  30.6%;  Pred. No. 3.65e-01;
  Matches    15;  Conservative   14;  Mismatches  18;  Indels   2;  Gaps   2;

Db      33 GILFSHPRDFTPVC-TTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLA 80
           | |  :| :|   |  |:|: :: ||:|   |   :::  |: ::||:|
Qy      45 GSLKWQPSNFIETCRNTQLAGSSELAAECKTRAQQFVSTKIN-LDDHIA 92


RESULT   12
ID   AOP2_HUMAN     STANDARD;      PRT;   223 AA.
AC   P30041; P32077;
DT   01-APR-1993 (Rel. 25, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   ANTIOXIDANT PROTEIN 2 (EC 1.11.1.7) (24 KDA PROTEIN) (LIVER 2D PAGE
DE   SPOT 40) (RED BLOOD CELLS PAGE SPOT 12).
GN   AOP2.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Miyajima N.;
RL   Submitted (MAR-1993) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   PARTIAL SEQUENCE OF 1-14.
RC   TISSUE=LIVER;
RX   MEDLINE; 93162045.
RA   Hochstrasser D.F., Frutiger S., Paquet N., Bairoch A., Ravier F.,
RA   Pasquali C., Sanchez J.-C., Tissot J.-D., Bjellqvist B., Vargas R.,
RA   Appel R.D., Hughes G.J.;
RT   "Human liver protein map: a reference database established by
RT   microsequencing and gel comparison.";
RL   Electrophoresis 13:992-1001(1992).
RN   [3]
RP   PARTIAL SEQUENCE OF 1-12.
RC   TISSUE=ERYTHROCYTE;
RX   MEDLINE; 94147970.
RA   Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
RA   Pasquali C., Sanchez J.-C., Tissot J.-D., Appel R.D., Walzer C.,
RA   Galant L., Hochstrasser D.F.;
RT   "Plasma and red blood cell protein maps: update 1993.";
RL   Electrophoresis 14:1223-1231(1993).
RN   [4]
RP   X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX   MEDLINE; 98246415.
RA   Choi H.J., Kang S.W., Yang C.H., Rhee S.G., Ryu S.E.;
RT   "Crystal structure of a novel human peroxidase enzyme at 2.0-A
RT   resolution.";
RL   Nat. Struct. Biol. 5:400-406(1998).
CC   -!- CATALYTIC ACTIVITY: DONOR + H(2)O(2) = OXIDIZED DONOR + 2 H(2)O.
CC   -!- SIMILARITY: BELONGS TO THE AHPC/TSA FAMILY. REHYDRIN SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; D14662; BAA03496.1; -.
DR   PDB; 1PRX; 17-JUN-98.
DR   SWISS-2DPAGE; P30041; HUMAN.
DR   PFAM; PF00578; AhpC-TSA; 1.
KW   Oxidoreductase; Peroxidase; Antioxidant; 3D-structure.
FT   INIT_MET      0      0
FT   ACT_SITE     47     47
SQ   SEQUENCE   223 AA;  24904 MW;  0B42C96F5CEBEFFC CRC64;

  Query Match           12.4%;  Score 85;  DB 1;  Length 223;
  Best Local Similarity  30.6%;  Pred. No. 3.65e-01;
  Matches    15;  Conservative   14;  Mismatches  18;  Indels   2;  Gaps   2;

Db      33 GILFSHPRDFTPVC-TTELGRAAKLAPEFAKRNVKLIALSIDSVEDHLA 80
           | |  :| :|   |  |:|: :: ||:|   |   :::  |: ::||:|
Qy      45 GSLKWQPSNFIETCRNTQLAGSSELAAECKTRAQQFVSTKIN-LDDHIA 92


RESULT   13
ID   ACHB_RAT       STANDARD;      PRT;   501 AA.
AC   P25109;
DT   01-MAY-1992 (Rel. 22, Created)
DT   01-MAY-1992 (Rel. 22, Last sequence update)
DT   15-DEC-1998 (Rel. 37, Last annotation update)
DE   ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
GN   CHRNB1 OR ACRB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=MUSCLE;
RX   MEDLINE; 91099317.
RA   Witzemann V., Stein E., Barg B., Konno T., Koenen M., Kues W.,
RA   Criado M., Hofmann M., Sakmann B.;
RT   "Primary structure and functional expression of the alpha-, beta-,
RT   gamma-, delta- and epsilon-subunits of the acetylcholine receptor
RT   from rat muscle.";
RL   Eur. J. Biochem. 194:437-448(1990).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; X74833; CAA52827.1; -.
DR   PIR; S13873; S13873.
DR   PFAM; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00254; NICOTINICR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Phosphorylation.
FT   SIGNAL        1     23       BY SIMILARITY.
FT   CHAIN        24    501       ACETYLCHOLINE RECEPTOR PROTEIN, BETA
FT                                CHAIN.
FT   DOMAIN       24    244       EXTRACELLULAR (POTENTIAL).
FT   TRANSMEM    245    269       POTENTIAL.
FT   TRANSMEM    277    295       POTENTIAL.
FT   TRANSMEM    311    332       POTENTIAL.
FT   DOMAIN      333    469       CYTOPLASMIC (POTENTIAL).
FT   TRANSMEM    470    488       POTENTIAL.
FT   DISULFID    151    165       BY SIMILARITY.
FT   CARBOHYD    164    164       POTENTIAL.
FT   MOD_RES     390    390       PHOSPHORYLATION (BY TYR-KINASES)
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FT                              (BY SIMILARITY).
SQ   SEQUENCE   501 AA;  57026 MW;  2E7DD6AAD1D9364D CRC64;

  Query Match           12.4%;  Score 85;  DB 1;  Length 501;
  Best Local Similarity  29.4%;  Pred. No. 3.65e-01;
  Matches    10;  Conservative   14;  Mismatches   7;  Indels   3;  Gaps   3;

Db    120 DGNFDVA-LDINVVV-SFEGSVRWQPPGLYRSSC 151
          :| :: : :|:| |: : :||::|||:  :  :|
Qy     26 NGGYNTSSIDLNSVIENVDGSLKWQPSN-FIETC 58


RESULT   14
ID   ACHB_HUMAN     STANDARD;      PRT;   501 AA.
AC   P11230;
DT   01-JUL-1989 (Rel. 11, Created)
DT   01-NOV-1995 (Rel. 32, Last sequence update)
DT   15-JUL-1998 (Rel. 36, Last annotation update)
DE   ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
GN   [illegible]HRNB1 OR CHRNB OR ACHRB.
OS   [illegible]omo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89296503.
RA   Beeson D.M.W., Brydson M., Newsom-Davis J.;
RT   "Nucleotide sequence of human muscle acetylcholine receptor
RT   beta-subunit.";
RL   Nucleic Acids Res. 17:4391-4391(1989).
RN   [2]
RP   VARIANT SCCMS MET-285.
RX   MEDLINE; 96256490.
RA   Gomez C.M., Maselli R., Gammack J., Lasalde J., Tamamizu S.,
RA   Cornblath D.R., Lehar M., McNamee M., Kuncl R.W.;
RT   "A beta-subunit mutation in the acetylcholine receptor channel gate
RT   causes severe slow-channel syndrome.";
RL   Ann. Neurol. 39:712-723(1996).
RN   [3]
RP   VARIANT SCCMS MET-289.
RX   MEDLINE; 97026281.
RA   Engel A.G., Ohno K., Milone M., Wang H.-L., Nakano S., Bouzat C.,
RA   Pruitt J.N. II, Hutchinson D.O., Brengman J.M., Bren N., Sieb J.P.,
RA   Sine S.M.;
RT   "New mutations in acetylcholine receptor subunit genes reveal
RT   heterogeneity in the slow-channel congenital myasthenic syndrome.";
RL   Hum. Mol. Genet. 5:1217-1227(1996).
CC   [illegible]!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC   [illegible]    EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- DISEASE: DEFECTS IN ACHRB ARE ONE OF THE CAUSES OF THE SLOW-
CC       CHANNEL CONGENITAL MYASTHENIC SYNDROME (SCCMS).
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; X14830; CAA32939.1; -.
DR   PIR; S04607; S04607.
DR   MIM; 100710; -.
DR   MIM; 601462; -.
DR   PFAM; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00254; NICOTINICR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Phosphorylation; Disease mutation.
FT   SIGNAL        1     23
FT   CHAIN         24    501       ACETYLCHOLINE RECEPTOR PROTEIN, BETA
FT                                 CHAIN.
FT   DOMAIN        24    244       EXTRACELLULAR.
FT   TRANSMEM     245    269
FT   TRANSMEM     277    295
FT   TRANSMEM     311    332
FT   DOMAIN       333    469       CYTOPLASMIC.
FT   TRANSMEM     470    488
FT   DISULFID     151    165       BY SIMILARITY.
FT   CARBOHYD     164    164       PROBABLE.
FT   MOD_RES      390    390       PHOSPHORYLATION (BY TYR-KINASES)
FT                                 (BY SIMILARITY).
FT   VARIANT      285    285       L -> M (IN SCCMS).
FT                                 /FTId=VAR_000287.
FT   VARIANT      289    289       V -> M (IN SCCMS).
FT                                 /FTId=VAR_000288.
SQ   SEQUENCE   501 AA;  56725 MW;  F8255BDE366A2A84 CRC64;

  Query Match           12.4%;  Score 85;  DB 1;  Length 501;
  Best Local Similarity  32.4%;  Pred. No. 3.65e-01;
  Matches    11;  Conservative   13;  Mismatches   7;  Indels   3;  Gaps   3;

Db    120 DGNFDVA-LDI-SVVVSSDGSVRWQPPGIYRSSC 151
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Qy     26 NGGYNTSSIDLNSVIENVDGSLKWQPSN-FIETC 58


RESULT   15
ID   ACHB_MOUSE     STANDARD;      PRT;   501 AA.
AC   P09690;
DT   01-MAR-1989 (Rel. 10, Created)
DT   01-MAR-1989 (Rel. 10, Last sequence update)
DT   01-NOV-1997 (Rel. 35, Last annotation update)
DE   ACETYLCHOLINE RECEPTOR PROTEIN, BETA CHAIN PRECURSOR.
GN   CHRNB1 OR ACRB.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 87057335.
RA   Buonanno A., Mudd J., Shah V., Merlie J.P.;
RT   "A universal oligonucleotide probe for acetylcholine receptor genes.
RT   Selection and sequencing of cDNA clones for the mouse muscle beta
RT   subunit.";
RL   J. Biol. Chem. 261:16451-16458(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE; 89214211.
RA   Buonanno A., Mudd J., Merlie J.P.;
RT   "Isolation and characterization of the beta and epsilon subunit genes
RT   of mouse muscle acetylcholine receptor.";
RL   J. Biol. Chem. 264:7611-7616(1989).
CC   -!- FUNCTION: AFTER BINDING ACETYLCHOLINE, THE ACHR RESPONDS BY AN
CC       EXTENSIVE CHANGE IN CONFORMATION THAT AFFECTS ALL SUBUNITS AND
CC       LEADS TO OPENING OF AN ION-CONDUCTING CHANNEL ACROSS THE PLASMA
CC       MEMBRANE.
CC   -!- SUBUNIT: PENTAMER OF TWO ALPHA CHAINS, AND ONE EACH OF THE BETA,
CC       DELTA, AND GAMMA (IN IMMATURE MUSCLE) OR EPSILON (IN MATURE
CC       MUSCLE) CHAINS.
CC   -!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
CC   -!- SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC CHANNELS FAMILY.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; M14537; AAA37154.1; -.
DR   EMBL; J04699; AAA37156.1; -.
DR   PIR; A25338; A25338.
DR   MGD; MGI:87890; ACRB.
DR   PFAM; PF00065; neur_chan; 1.
DR   PRINTS; PR00252; NRIONCHANNEL.
DR   PRINTS; PR00254; NICOTINICR.
DR   PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
KW   Receptor; Postsynaptic membrane; Ionic channel; Glycoprotein; Signal;
KW   Transmembrane; Phosphorylation.
FT   SIGNAL        1     23
FT   CHAIN        24    501       ACETYLCHOLINE RECEPTOR PROTEIN, BETA
FT                                 CHAIN.
FT   DOMAIN        24    244       EXTRACELLULAR.
FT   TRANSMEM     245    269
FT   TRANSMEM     277    295
FT   TRANSMEM     311    332
FT   DOMAIN       333    469       CYTOPLASMIC.
FT   TRANSMEM     470    488
FT   DISULFID     151    165       BY SIMILARITY.
FT   CARBOHYD     164    164       PROBABLE.
FT   MOD_RES      390    390       PHOSPHORYLATION (BY TYR-KINASES)
FT                                 (BY SIMILARITY).
SQ   SEQUENCE   501 AA;  56930 MW;  787BDDA90EBB0EF2 CRC64;

  Query Match           12.4%;  Score 85;  DB 1;  Length 501;
  Best Local Similarity  29.4%;  Pred. No. 3.65e-01;
  Matches    10;  Conservative   14;  Mismatches   7;  Indels   3;  Gaps   3;

Db    120 DGNFDVA-LDINVVV-SFEGSVRWQPPGLYRSSC 151
          :| :: : :|:| |: : :||::|||:  :  :|
Qy     26 NGGYNTSSIDLNSVIENVDGSLKWQPSN-FIETC 58


Search completed: Wed Aug 16 09:45:13 2000
Job time : 8 secs.
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